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GenCore version 5.1.3
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OM protein - protein search, using sw model

Linuary 16, 2003, 16,39,12 , Scarch time 20.4 Seconds Run on

(without alignments) 28.464 Million cell updates/sec

1 EREKEOMMREKEEL 14 US-09-856-070-17 Perfect score: Sednence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Tetal number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues

Minimum DB seq length: 6 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100% Maximum Match 100% Listing tirst 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rosii †		> - - - -				
NO.	Score	Match	Length	DB	ID	Description
П	69	100.0	580	-	EZRI_BOVIN	P31976 bos taurus
C a	5.3	100.0	585	- 4	ELEKT HOMAN	1 homo
ĸ	99	95.7	ባ የ		EVR ! MOIISP	P26040 mus musculu
4	51	73 9	576	,	MOES HUMAN	H.H
വ	51	73.9	576	7	MOES_MOUSE	Ξ
9	51	÷	576	_	MOES_PIG	P26042 sus serrofa
7	51	73.9	583	_	PADI_HIMAN	P35241 homo sapien
œ	5.1	73.9	583	_	RADI_MOUSE	_
6	5.1	73.9	583	_	RAD1_P1G	P26044 sus serofa
10	47	68.1	1549	-	TPHY_SHEEP	P22793 ovis aries
11	46	F. A.A.	2564	_	SPOO_HTIMAN	Q9h254 homo sapies
15	€ ₹	æ. G	321		ABRA_FIAFF	plasm
13	43	62.3	743	1	ABPA_P! AFC	F22520 plasmodium
14	43	62.3	1157	_	Y182_HUMAN	
1.5	43	62.3	1344		1F3A_MOUSE	P23116 mus musculu
16	43	62.3	1382	٠.	1F3A_HUMAN	homo
17	43	62.3	1407		TPHY_PARIT	OEY^{C}
18	۲ 7	6.24	1898		TPHY_HIMMAN	
19	4.2		123	1	RBFA_NEIMA	Q9jtx7 neisseria m
CI	4.2	6.00	123	٠.	FRFA_NIT MB	$09j_{TT}^{-2}$ neisseria m
21	42		216	-	ERP6_YEAST	P53198 saccharomyc
23	4.2		471	_	YAL5_SCHPC	QU9928 schizosacch
53	4.2	60.9	514		ZRF1_MOUSE	P54103 mus musculu
₹ (1	42	¢ (9	4687	-	FLE1_RAT	P30427 rattus norv
25	4 1	59.4		-	IATF_YEAST	P01097 saccharomyc
35	41	59.4	243		TRIC_XPNLA	P50754 xenopus lae
27	41	59.4			NESG_HUMAN	Qqull6 homo sapien
28	41	59.4	419		NEMO_HUMAN	h nf-
58	4 1	59.4	476	_	MPPB_NEUCR	Plidl3 neurospora
UŁ	4.1	4	877	_	INCE_CHICK	
31	4	59.4	2068	٦	T2D1_DROME	drosc
32	40	5.8	180	_		P53801 homo sapten
33	40	58.0	249	_	PSE1_MOUSE	mus m

Structural protein, Cytoskeleton, Phosphorylation.

INIT

	40	0.895	462	_	MPPB YEAST	P10507 Saccharomyo
35	40	58.0	466	-	CYP8_CAEEL	P52016 caenorhabd
	40	58.0	503	-	CP39_RAT	P51538 rattus nor
	40	58.0	503	-	CP3D_MOUSE	Q64464 mus muscul
~	40	58.0	592	-	GBP1_HUMAN	P32455 homo sapie
œ	40	58.0	1959	,	MYH9 CHICK	P14105 dallus dal
0	40	58.0	1960	_	MYH9_HUMAN	P35579 homo sapic
11) †	0.83	4473	_	PLET_CRICK	09ji55 cricetulus
~1	36	56.5	148	-	SSRP_RALSO	Q8xzhl ralstonia
œ	6 e	56.5	508	-	MAT1_XENLA	P51951 xenopus la
_	39	56.5	330	_	RLX3_STAAU	P14491 staphylocod
10	OT:	56.5	341	,	12D6 MOUSE	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@lsb sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bergson C.M., Zhao H., Saijoh K., Duman R.S., Nestler E.J.;
Exrith and Ostconcetin, two proteins associated with cell shape and
growth, are enriched in the locus cocruleus.";
Mol. Cell. Neurosci. 4:64-73(1993).
                                                                                                                                                                                                   Eukaryota, Metazoa, Phordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURES TO THE PLASMA MEMBRANE.
-1- SÜRCELLÜLAR FOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN (CYTOPLASMIC SIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PIM: PHOSPHOPYLATED BY PROTEIN-TYROSINE KINASES.
                                                                                                                        01-701-1993 (Rel. 26, Last sequence update)
16 OCT 2001 (Rel. 40, Last annotation update)
ALIGNMENTS
                                                                                                                                                      Ezrin (p81) (Cytovillin) (Villin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000299; Band_4.1.
InterPro, IPR003738, Ez/rad/moesin.
                                                                                                                                                                                                                                                                                                                                                                                                           IISSUE-Kidney;
MEDLINE 96239137; PubMed-8660651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PSOUSEO: BAND_41_1; 1. PROSITE: PSOUSE1; BAND_41_2; 1. PROSITE: PS50057; BAND_41_3; 1.
                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-THL-1993 (Rel. 26, Last seq
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-15 AND 126-140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00373; Band_41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M98498; AAA30510.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS: PR00935; BAND41.
SMART; SM00295; B41; 1.
                                                                          STANDARD;
                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00769; ERM; 1.
                                                                                                                                                                                       Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   NCB1_TaxID-9913;
                                                                       EZRI_BOVIN
F31976,
                                                           ECRI_BOVIN
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Samelson L.E.,
"Identification of exin as an 81-KDa tyrosine-phosphotylated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Turunen O., Winqvist P., Pakkanen P., Grzeschik K.-II., Wahlstroem T.,
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Egerion M , Moritz P I , Druker B , Kelso A , Simpson P I ;
"Identification of the 70kb heaf shock cognate protein (Hse70) and
alpha-actinin-1 as novel phosphotyrosine containing proteins in T
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazba, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krieg J., Hunter T.; "Identification of the two major epidermal growth factor induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Offenwaelder B., Obermaler B., Mewes H. W., Weil B., Wiemann S., Submitted (MAR-2000) to the EMBL/GenBank/10BJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cytovillin, a microvillar Mr 75,000 protein, chNA sequence, prokaryotic expression, and chromosomal localization."; J. Biol. Chem. 264:16727-16732(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gould K.L., Bretscher A., Esch F.S., Hunter T.; "cDNA cloning and sequencing of the protein-tyrosine kinase substrate, ezrin, reveals homology to band 4.1.";
                                                                                                                  100.0%; Score 69; DB 1; Length 580;
                                                                                                                                                  0; Indels
              PHOSPHORYLATION (BY PDGFR)
                                                 PHOSPHORYLATION (BY PDGFR)
                                                                                  ECD663E5C200FAA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem, Biophys Pes Ocamus 224-666-674(1996)
                                                                                                                                Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                    P15311; P23714; G9NSJ4; 01-APP-1440 (Fel. 14, Created) 01-NoV-1991 (Rel. 20, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                 (BY SIMILARITY).
                                                                (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                          585 AA
                                                                                                                                                    0; Mismatches
BAND 4.1-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90076135; Pubmed-2591371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chem 267-19258-19265(1992)
                                                                                                                                                                                                                                                                                                                                                                                            Ezrin (p81) (Cytorillin) (Villin 2).
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| Hd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92388649; PubMed-1381389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIJINE-92406868; PubMcd-1382070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 171-179 AND 342-349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in T cells.";
J. Immunol. 149:1847-1852(1992).
                                                                                  580 AA; 68629 MW;
                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 8:4133-4142(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION BY PDGFR.
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                       333 EREKEÇMMREKEEL 346
                                                353
                                                                                                                                                                                      1 EREKEOMMREKEEL 14
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ymphocytes.
                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                          EZRI_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaheri A.;
                                                                                SEQUENCE
                                                                                                                  Query Match
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                MOD_RES
                                                 MOD_RES
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                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92064635; PubMed-1955455;
Funayama N., Nagafuchi A., Sato N., Tsukita S., Tsukita S.;
"Radixin is a novel member of the band 4.1 lamily.";
A. Cell Biol. 115:1039-1048(1991).
FUNCTION: PROHABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL. SIRUCTURES TO THE PLASMA MEMBRANE. SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukaryota: Modaroa; Chordata: Craniata: Vertebrata: Enteleostomi;
Mammalia: Eutheria: Rodentia: Sciuroquathi; Muridae; Murinae: Mus.
                                                      (CYTOPLASMIC SIDE).
TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 69; DB 1; Length 585; 100.0%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY PDGFK).
PHOSPHORYLATION (BY PDGFK).
V -> [ (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> 1. (IN REF. 3).
2A844D140E3B06CC CRC64;
                                                                                                             PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES. SIMILAKITY: CONTAINS 1 HAND 4.1-1.1KE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00660; HAND_41_1; 1.
PROSITE; PS00661; BAND_41_2; 1.
PROSITE; PS00657; BAND_41_3; 1.
Structural protein; Cytoskeleton; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01 MAY 1992 (Rel. 22, Created)
61 MAY-1992 (Rel. 22, Luot sequence updute)
16-007-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAND 4.1-1.1KE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                            EMBL; AL162086; CAB82418.1; ALI_INIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ezrin (p81) (Cytovillin) (Villin 2).
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                                                                                                                                                                                                                                                                                                                                         1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; iPR000299; Band_4.1.
InterPro; iPR006798; Ez/rad/mo
Plam; PP00783; Band_41; 1.
Plam; PP00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585 AA; 69267 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-2DPAGE; P15311; HUMAN.
                                                                                                                                                                                                                                                                                                                       EMBL; X51521; CAA35893.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR00935; BAND41.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Genew: HGNC:12691; VII.2.
MIM: 123900; -.
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                                                                                                                                                                                                                                                                                                                                           J05021; AAA61278.
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                                                                                              EPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                            PIR; S09263; S09263.
PIR; A34400; A34400.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EZRI_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A gene family consisting of earin, radixin and mossin. Its specific localization at actin filament/plasma membrane association sites."; J. Cell Sci. 103.131 143(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Elkaryota, Metalou, Cherdati, Chariata, Vertebilita, Euteleostomi:
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sato N., Funayama N., Nayafuchi A., Yonemura S., Tsukita S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.9%; Score 51; DH 1; Length 576; 71.4%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94CE7C28D55A8176 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FBB-1994 (Rel. 28, Last sequence update)
16-9cT-2001 (Rel. 40, Last annotation update)
Moesin (Membrane-organizing extension spike protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURES TO THE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAND 4.1-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                        PRINTS: PR00935; BAND41.
SAMET: SM00035: BAND41.
PPOSITE: PS00660: BAND-41.1.
PPOSITE: PS00661: WAND-41.2: 1.
PROSITE: PS00657: HAND-41.3: 1.
PROSITE: PS00057: HAND-41.3: 1.
INT_MET
                                                                                                                                                                                                                                                                         InterPro: IPE000299; Band_4.1.
InterPro: IPR000798; Ez/rad/moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MESSINE-93055012; FubMcd-1429901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
                                                                                                                                                                                                      Aarhus/Ghent-20PAGE: 3515; IEF
Aarhus/Ghent-20PAGE: 3516; IEF
Genew, HGNC.7373, MSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STE AN: 67689 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kidney Int. 41:665-670(1992).
                                                                                                                                                EMBL, M69066, AAA36302.1; -.
EMBL: 298946; CAR46379 1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            role in cellular functions.
                                                                                                                                                                                                                                                                                                           Pfam; PF00373; Band_41; 1.
Pfam: PF00769; ERM: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 EKEKEKLEREKEEL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EREKEOMMREKEEL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1)
(1)
                                                                                                                                                                                         P!R; A41289; A41289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
                                                                                                                                                                                                                                                       MIM; 309845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MORS_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsukita S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEČITENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOES_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-1999) to the EMBL/Genhank/DubA databases.
-!- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKFLFTAL.
-!- STRUCTURES TO THE PLASMA MEMBRANE.
-!- TISSUE SPECIFICITY: IN ALL TISSUES AND CHLTHRED CELLS STUDIED.
-!- SIMILARITY: CONTAINS I BAND 4.1.LIKE DOMAIN.
-!- DATABASF: NAME-Atlas Genet Cytogenet Opnos!, Hacematel.;
WWW-"http://www.infoblogen fr/services/chromcancer/Genes/MSNID363.htm!".
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O
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Proc Natl Arad Sci. H.S.A. 88-8297-8301(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryola, Melazoa, Chordata, Craniata, Vertebrata, Futeleostomi;
Mammalia, Eutheria; Primates; Catarihini; Hominidae; Homo
 -!- TISSUE SPECIFICITY: COMPONENT OF THE MICHOVILL OF INTESTINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N A , AND SEQUENCE OF 1-15; 53-59 AND 413-434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.7%, Score 66; DB 1; Length 585; 92.9%; Pred. No. 0.036; Live 1; Mismatches 0; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY PDGFP) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY PDGFR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
2057EDEDEDBOSSDD CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rcl. 22, Created)
01-MAV-1992 (Rcl. 23, Last sequence update)
15-JUN-2002 (Pcl. 41 Last annotation update)
Moesin (Membrane-organizing extension spike prolein).
                              -1- PIM- PHOSPHOPYLATED BY PROTEIN-TYPOSINE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                              Structural protein; Cytoskeleton; Phosphorylation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAND 4.1-LIKE
                                                                                                                                                                                                                                     PIR: B41129; B41129.
MaD: MG1-98941, VILL2.
InterPro: IPRO00299; Hz/rad/mocsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92020840; PubMod-1924289;
                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PSONGGO: BANK 41 1: 1
PROSITE: PSONGGI; BANK 41 2; 1
PROSITE: PS50057; BANK 41 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    585 AA, 69214 MW,
                                                                                                                                                                                                                        EMBL; X60671; CAA43386.1; -
                                                                                                                                                                                                                                                                                                         Pfam; PF00373; Band_41; l.
Pfam; PF00769; ERM; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ankes W.T., Furthmayr H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00935; BAND41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 EREKEOMLREKEEL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EREKEQMMREKEEL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                            SM00295; B41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 13, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_Tax1D-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
                                                                                                                                                                                                                                                                                                                                                                                                                                                0 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Howden P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P26038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOES_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94092743; FubMed 8268231; Lankmayr H., Lanksow M.T., Schwartz Albiez R., Furthmayr H., Cloning and sequencing of portine meesin and radixin chNA and identification of highly conserved domains."; Biochim. Biophys. Acta 1226:497-482(1993).

-1- FUNCTION: PROBARY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL STRUCTION: THE PLANAMA MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.9%; Score 51; DB 1; Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5E0F455552E9145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Mci. 22, Created)
01-MAT0-1992 (Mci. 23, Last Sequence update)
16-0CT-2001 (Mci. 40, Last amnotation update)
Moesin (Membrane organizing extension spike protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                    EL -> DV (IN REF. 2).
RA -> SP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY,
BAND 4.1-LIKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3.9; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                   InterPro; IPR000299; Band_4.1.
InterPro; IPR000798; Ez/rad/moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; 1PR000798; Ez/rad/moesin.
                                                                                                                                                                                                                                                                                                                                                                              Structural protein; Cytoskeleton.
                                                                                                                                                                                                                                                                                                                PROSITE: PS00660; BAND_41_1; 1. PROSITE: PS00661; BAND_41_2; 1. PROSITE: PS50057; BAND_41_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           576 AA; 67635 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000299; Band_1.1.
                                                                                                                        EMBL; S47577; AAA11762.1; -. EMBL; M86390; AAA39728.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M86450; AAB02864.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.48;
                                                                                                                                                                                                                              Ptam; PF00373; Band_41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00373; Hand 41; 1.
Ptam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                 Ptam; PE00769; ERM; 1.
PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 EKEKEKIEREKEEL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00935; BAND41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EREKEQMMREKEEL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                          175
                                                                                                                                                                   MGD; MG1:97167; Msn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      3.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                          370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus serota (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                               INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOES_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
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-!- FINCTION - CHOCKAUTY PLAYS A CPUCIAL FOLE IN THE HINDING OF THE BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.

-!- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERGUAT OF THE CELL-TO-CELL ADDRESS, BRINTION AND THE CLEAVAGE FURROW IN THE INTERHASE AND MITOTIC PHASE, RESPECTIVELY.
-!- SIMILARLIY: CONTAINS 1 HAND 4.1-1.1KE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                GdFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilgenbus K.K., Milatovich A., Francke U., Furthmayr H.;
"Molecular cloning, cDNA sequence, and chromosomal assignment of the
human radixin gene and two dispersed pseudogenes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Structural profess, Cytoskeleton, Actin-binding, Capping profess.
DOMAIN 58 225 BAND 4.1-LIKE.
                                                                                                                                                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                                                                                      73.9%; Score 51; DB 1; Length 576; 71.4%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                     BAND 4.1-LIKE.
3CEUBE/8E5F75E6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            889687E1D675FFE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01 FBF:1994 (Ref. 28, Created)
01-FEB-1994 (Ref. 28, Last Sequence update)
16-0CT-2001 (Ref. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                             BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY - PRO .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR000299; Band_4.1.
InterPro: IPR000798; Ez/rad/moesin.
                    PROSITE: PS00660; BAND 41_1; 1.
PROSITE: PS00661; BAND 41_2; 1.
PROSITE: PS50057; BAND 41_3; 1.
Structural protein; Cytoskeleten.
INIT_MET 0 0 BY S.
DOMAIN 57 224 BAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93252378; PubMcd-8486357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS00660; BAND_41_1; 1. PROSITE: PS00661; BAND_41_2; 1. PROSITE: PS50057; BAND_41_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A46127; A46127.
Aarhus/Ghent-2DPAGE; 2501; IEF
                                                                                                                                                          INIT_MET 0 0 B
DOMAIN 57 224 B
SEQUENCE 576 AA: 67529 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68564 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L02320; AAA36541.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00373; Band_41; 1.
                                                                                                                                                                                                                                                                                                                        Local Similarity 71.4
bes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS: PR00935; BAND41.
SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 EKEKEKIEREKEEI, 346
SMART: SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      1 EREKEOMMREKEEL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew: HGNC:9944; RDX.
MIM: 179410; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00769; ERM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     583 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470
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                                                                                                                                                                                                                                                                                      Query Match
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   A PERSONAL PROPERTY OF THE CONTRACT OF THE CON
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SEQUENCE FROM N.A
   P26044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ċ
                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERGOAT OF THE CELL-TO-CELL ADHERENS LITHNATION AND THE CLEAVASE FURROW IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                         SUCE
                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Motaλoa, Chorddia, Craniata, Vertebrata, Euteleostomi).
Mammalia, Eutheria, Rodentia, Sciuroquathi, Murinae, Musinae; Mus
                                                                                                                                                                                                                                                                                                 Funayama N., Nagatuchi A., Sato N., Tsukita S., Tsukita S., "Padixis is a neyel member of the band 4.1 family", J. Cell Biol. 115-1079-1048(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00660; BAND_41_1; 1.
PROSITE: PS00661; BAND_41_2; 1.
PROSITE: PS00657; BAND_41_3; 1.
Structural protein; Cytoskeleton; Actin-binding; Capping protein.
DOMAIN 58 225
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C
73.9%; Score 51; FB 1; Length 583; 71.4%; Pred. No. 4; attive 3: Mismatches 1; Indols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51, DB 1, Length 583,
Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                               BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.
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                                                                                                                                                                                                                                                                   SEQUENCE FROM N A., AND SEQUENCE OF 28-53 AND 263-277
                                                                                                                                                                                                                                                                                                                                                                                 INTERPHASE AND MITOTIC PHASE, RESPECTIVELY -!- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
                                                                                                                                               01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   583 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY - PRO
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MG1-97887; PdX.
InterPro, 1PR000299; Band_4.1.
InterPro, 1PR000299; Band_4.1.
Pfam; PP00373; Band_41; 1.
Pfam; PP00373; Band_41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                      MEDIINE-92064635, PubMed-1955455,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.98;
71:48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Xbub72; CAA4 COR7 1;
                      10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00935; BAND41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                   334 EKEKERIEREKEEL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 EKEKERIEREKEEL 347
                                             1 EREKEQMMREKEEL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART, SM00295, B41, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ERRKROMMREKEEL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A41129; A41129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
            Local Similarity
                                                                                                                                                                                                                                            NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
470
                                                                                                                           RADI_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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ID RADI_PIG
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  Query Match
                                                                                                                                                                                    Padixin
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                                                                                                                 RADI_MOUSE
                      Matches
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                                                                                                                                                                                                                                                                     Salis
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                    Bukaryota; Metazoa; Chordata; Cramiata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structural protein; Cytoskeleton; Actin-binding; Capping protein.
DOMAIN 58 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 1, Length 583;
Pred. No. 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              583 AA; 68549 MW; 59AEA286DCAF7397 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPHASE AND MITCHIC PHASE, RESPECTIVELY.
-!- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
0] MAY 1992 (Rel. 22, Created)
0] MAY-1992 (Fe] 22, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
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15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000798; Hz/rad/moesin.
Pfam; PF00373; Band_41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHINTS, FR00935, BAND41, SMAPT: SM00295, B41; 1, PPROSETP: PS00666, BAND41_1; 1, PROSETP: PS00961; HAND 41_2; 1, PROSETE; PS50057; BAND41_2; 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P227<u>9</u>3;
01-AUG-1991 (Rel. 19, greated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000299; Band_4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.98,
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; MWh444; AABU2865.1; -.
PIP; S39805; S39805.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EREKEÇMMREKEEL 14
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Host Local Similarity
Host Local Conserva
                                                                              Radixin (Moesin B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                               Sus scrofa (Pig)
                                                                                                                                                                                                      NCBI_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470
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Fictz M.J., McLaughlan C.J., Campbell M.T., Rogers G.E.; "Analysis of the sheep trichohyalin gene: potential structural and calcium binding roles of trichohyalin in the hair follicle.";
MEDIJINE-93260018; PubMed-7684041
                                                                                                                                                                                         cell Biol. 121:855-865(1993).
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SEQUENCE OF 1016-1549 FROM N.A. SIRAIN-MOTINO-DOISEL BOIN X ROIDOI LAIGASEEL, TISSUE-WOOL FOLLICIES. MEDLINE-90130632; PubMed-2298812;

Fielz M.J., Presland R.B., Rogers G.E., The cDNA-deduced amino acid sequence for trichohyalin, a differentiation marker in the hair fellicle, centains a 23 amino acid

repeat."; J. Cell Biol. 110:427-436(1990)

FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN RESULTABA ARRAYS WITH REPARTIN INTERMEDIATE FILAMENTS (FIF) OF THE INNER ROOT SHEATH CELLS OF THE HATE FOLLICLE AND THE GPANULAR LAYER OF THE EPIDERMIES, IT LATER BECOMES CROSS-LINKED TO KIF HY ISODIPEPTIDE BONDS. IT MAY SEXVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CFIT ENVELOPE OF EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DUPING TEPMINAL DIFFERENTIATION.

SUBUNIT: HOMODIMER (PROBABLE).

ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS MAY HE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE TISSUE SPECIFICITY: FORDO IN THE BARD KERATINIZING TISSUES SHORT SHEATH (IRS) OF BAILFOLLES AND MEDULLA. AND IN THE EDITHELIA OF THE TONGUE, HOOF AND RUMEN.

-!- DOMAIN: CONSISTS OF NINE DOMAINS, DOMAIN T CONTAINS TWO PF-HAND CALCTUM-BINDING DOMAINS DOMAINS 2-4. 6, AND R ARE ALMOST ENTIRELY ALPHA-HELLCAL, CONFIGURED AS A SERIES OF PEPTIDE REPRATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHALLOLA ROD STABILLIZED BY TONIC INTERACTIONS POWAIN 6 IS THE WOST REGULAR AND MAY RIND KIF DIPECTLY BY LONIC INTERACTIONS. DOMAINS 5 AND 7 ARE LESS WELL, ORGANIZED AND MAY INDUCE FOLDS IN DOMAIN 9 CONTAINS THE C-TERMINGS, CONSERVED AMONG DIFFERENT SPECIES. THE MOLECULE.

PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE. SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO THE S-100 SOME 200 APGININES APF SUBSTRATE OF TPANSGLUTAMINASE

SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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RESULT 11

EF-HAND 1 (LOW AFFINITY) (POTENTIAL). EF-HAND 2 (HIGH AFFINITY) (POTENTIAL). 14 X 28 AA APPROXIMATE TANDEM REFEATS. Pfam: PF00036; efhand; 1. Ptam: PF01002; S.100; 1. ProDom: PD003407; CaBP_S100; 1. PROSITE: PS000408; FF_HAND; 1. InterPro; IPR001751; CaBP_S100. InterPro; IPR002048; EF-hand. EMBL; X51695; CAA35992.1; EMBL: 218361; CAA79165.1; PIR; A40691; A40691. PIR; A34209; A34209. PIR; 532644; 542633. 11G5 HSSP; P02633; CA_BIND DOMAIN KEPEAT REPEAT REPEAT ᄎᆇᆂᆸᆸᇫᆇᇫᅔᅔᆇᆇᇀᆂᆂᆂᆍᆓᆓᆓᆓᆍᆍᆍᇸᆇᆂᆂᄪᆖᆸᇤᆴᇎ

7 - (1.6.		œ	1-9.	1-10.	1-11.	1-12.	1-13.	1-14	23 X 23 AA APPROXIMATE LANDEM REPEATS.		. cı	2-3.	2-4.	2-5,	2-6.	2-7.	2-8.	2-9.	2-10.	2-11.	2,12.	2-13,	2-14.	2-15.	2-16.	2-17.	2-18.	2-19.	2-20.	2-21.			CIN SHORT	MISSING (IN SHORE FORM).	E 17 G (IN REF. 2). MW: E7DERGEE12DGERAE ORGGA:	Score 47; DB 1; Length 1549;	red. No. 37;	5; Mismatches 0; Indels 0; Gaps			
532	560	588	616	644	678	706	742	771	796	832	1507	961	388	1021	1044	1067	1090	1121	1144	1167	1197	1227	1250	1273	1296	1319	1342	1368	1391	1416	1439	1461	1484	1507	1197	0.00	1399 AA: 201173	68.18;		rvative	1. 14	1	L 1184
505	533	561	583	617	645	679	707	743	772	797	938	938	662	986	1055	1045	1068	1041	1122	1145	1158	1198	1228	1251	1274	1297	1320	1343	1369	1392	1417	1440	1462 1462	Ω ••••••••••••••••••••••••••••••••••••	1145	0000	1040		imilarit _	Conservat	REKEOMMREKEET.		REEEÚLLÚEREEL
REDEAT	REPEAT	DOMAIN	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	REPEAT	PEPEAT	REPEAT	VARIANT	VARIANI	SECUENCE	Query Match	Rest Local Similarity	teres 8,	2 REKE		1172 REEE																					
Ξ	Ξ	FT	FT	FI	ĽН	H	도	FT	FT	LJ	E	H	FT	F.	ΕŢ	LJ	FT	7	ī.	E.	E.	Ld	Ξ.	£. 1.	Ľ.	FI	F.	FT	긒	FI	Ξ	FT	E→ :	1.1	<u>.</u>	: !	ī, õ	no O	æ:	Ma	:-	ì	qq

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"A new spectrin, beta-IV, has a major truncated isolorm that associates with promyelucytic leukemia protein nuclear bodies and the nuclear matrix.";
                                                                                                                                                                                                 Spectrin beta chain, brain 3 (Spectrin, non-erythroid beta chain 3) (Beta-IV Spectrin).
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa; Cherdata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1se W.T., Tang J., Jin O., Korsgren C., John K.M., Kund A.L.,
Gwynn B., Peters L.L., Lux S.E.;
                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                   Q9H354: Q9HCDD: Q9H3GB: Q9H1K7: Q9H1K8: Q9H1K9:
15-JUN-2002 (Rel. 4], Created)
15-JUN-2002 (Rel. 4], Last sequence update)
15-JUN-2032 (Rel. 4], Last annotation update)
                                  2564 AA
                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21316449; PubMed-11294830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                   SPIBN4 OR SPIBN3 OR KIAA1642.
                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9606;
                               SPCQ_HUMAN
SPCQ_HUMAN
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Chem. 276:23974-23985(2001).

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                                                                                                                                                                                                 Nagase T., Kikuno B., Nakayama M., Hirosawa M., Obera C.:
"Prediction of the coding sequences of unidentified human genes.
XVIII. The complete sequences of 100 new cDNA clones from brain which
code for large professin vitro ":
DNA Res. 7:273-281(2000).
                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4, are
                                                                                                                                                                                                                                                                                                   produced by alternative splicing. --- TISSUP SPECIFICATY. Abundantly expressed in brain and pareteatic
                                                                                 "BetalV spectrin, a new spectrin localized at axon initial segments and nodes of ranvier in the central and peripheral nervous system."; a cell Hiol 151.495-1002(2000)
SEQUENCE FROM N.A. (ISOFORMS 1 TO 4).
MEDLINE-20539976; Pubmod-11086041;
Berghs S., Agqujaro D., Dirkx P. Tr., Maksimova E., Stabach P.,
Hermel T.-M., Zhang J.-P., Philbrick W., Slepnev V., Ort T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE: PS50003; PH_DOMAIN: 1.
Cytoskoleton, Membrane, Repeat, Actin-binding, Capping protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIN-BINDING (BY SIMILARITY)

    SIMILARITY: CONTAINS 2 CALPONIN-BOM-DESY (CH) DEMAINS
    SIMILARITY: CONTAINS 1 PH DOMAIN.

                                                                                                                                                                                                                                                                                                                                                  -!- SIMILABITY: BELONGS TO THE SPECTRIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: CONTAINS 18 SPECTRIN REPEATS.
                                                                                                                                                  SEQUENCE OF 386-2382 FPOM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
SPECTRIN 6.
SPECTRIN 6.
SPECTRIN 7.
SPECTRIN 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001589; Actbind_actnin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR001715; Calponin-like.
InterPro; IPR001849; PH.
                                                                                                                                                                                MEDLINE-29450683; PabMod 10997877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002017, Spectrin.
InterPro; IPR001605, Spectrin_PH.
Pfam; PF00169; PH: 3.
Pfam; PF00307; CH: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00150; SPEC; 16.
PROSITE: PS00019; ACTININ_1: 1.
PROSITE: PS00020; ACTININ_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF311855; AAG42473.1; --
EMBL; AF082075; AAC38874.1; --
EMBL; AY004226; AAF93171.1; --
EMBL; AY004226; AAF93172.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB046862; BAB13468.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00683; SPECTRINPH.
SMART; SM00033; CH; 2.
SMART; SM00233; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piam; PF00435; spectrin; 56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP: Q01082; 1BKR.
Genew; HGNC-14896; SPTHN4
MIM: 606214; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: AY004227; AAF93173.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alternative splicing.
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                                                                   Solimena M
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   THIRTHHELHER ARBENER BENER BENER BENER BENER BENER BOOCCOCCOCCOCC GOOCLER FRANKE BANKE FRANKE
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                                                                                                                                                                                                                                                                        SATSLATETPOTOGERARHK (IN ISOPOKM 3).
NUSMOLKADUWMOMINIQUH -> CELIHPALLHPPWE PPYLPRSSS (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
IEKTKARESTREPETPUTOFFFFORTELEARKAAFLLEFSGY E -> PREDHINPOVOLOGIWQHENPSLARKANKEKTAR ROGFORM 4).
MISSING (IN ISOFORM 4).
MISSING (IN ISOFORM 4).
                                                                                                                                                                                                                                                       AVQAAUCILLRÜCNIYÜLQAQLAVIRILLIK - MPHYPSÜS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Stahl H.-D., Blanco A.E., Crewther P.E., Anders R.F., Kyne A.P.,
Coppel R.L., Mitchell G.F., Kemp D.J., Brown G.V.;
"Sorting large numbers of clones expressing Plasmodium falciparum
antigens in Escherichia coli by differential antibody screening.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . BLOL. Med. 3:351-368(1986).
SUBCELLULAR LOCATION: AT THE MEPOZOTIF SUPFACE AND WITHIN THE PARASITOPHOROUS VACUOLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV 1991 (RCT. 20, Last sequence update)
01-FFB 1994 (RCT. 28, Last annotation update)
101 KDa malaria antigen (P101) (Acidic basic repeat antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum (isolate PC27 / Papua New Guinea).
Eukaryota, Aiveolata, Apicumpiexa, Haemosporida, Plasmodium.
NCBL_TaxiD-5837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1, Length 2564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPONEZDITUBUIEGO CROS4;
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                                                                                                                                                                                                                                  MISSING (IN ISOFORM 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L -> S (IN REF. 2).
E > K (IN REF. 2).
E -> K (IN REF. 2).
G -> S (IN REF. 1).
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SPECTRIN 10.
SPECTRIN 11.
SPECTRIN 12.
SPECTRIN 12.
SPECTRIN 13.
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SPECTRIN 16.
SPECTRIN 16.
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SPECTRIN 17.
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64.38;
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P23746;
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                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88298794; PubMed-3042768; Weber J.L. Lyon T A., Woltt P H. Hall T.. Lowell G.H., Chulay J.D., "Primary structure of a Plasmodium falciparum malaria antiqen located at the merozoite surface and within the parasitophorous vacuole."; J. Hiol. Chem. 263:11421-11425(1988).
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                                                                  Caps
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                                                                                                                                                                                                                                                                                          101 kDa malaria antigen (P101) (Acidic basic repeat antigen).
                                                                                                                                                                                                                                                                                                                                           Eukaryota: Alveolata: Apiromphexa: Haempsporida: Plasmodium
                              62.3%; Score 43; DB 1; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.3%; Score 43; DB 1; Length 743; 61.5%; Pred. No. 62; tive 3; Mismatches 2; Indels
                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANDEM REPEATS OF K-E(2,3). FBF0B0F8B07D922C CRC64;
37805 MW; QRRH4A0681P0714B CPC64.
                                                                                                                                                                                                                                                                                                                          Plasmodium talciparum (isolate Camp / Malaysia)
                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                            743 AA
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01-NOV-1997 (Rel. 35, Last sequence update)
                                                              3; Mismatches
                                             Pred No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       !- PTM: NOT GLYCOSYLATED (PROBABLE).
                                                                                                                                                                                                            PPT:
                                                                                                                                                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86622 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J03902; AAA29462.1; -.
                                            61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPASITOPHOROUS VACUOLE.
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen; Malaria; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                            STANDAPD
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                                                                                                                             290 EKEKEEKEKEE 302
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                                                                                             1 EREKEQMMREKEE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EREKEQMMREKEE 13
321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A29232; A29232.
                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            743 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hest Logal Similarity
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          NCB1_Tax ID-5835;
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268
674
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238
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20
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Q14687;
SECUIENCE
                              Query Match
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                                                              Matches
                                                                                                                                                                                              ABRA PLAFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fetzelt C., Joswig G., Mincheva A., Lichter P., Stammer H., Werner D., "The centrosomin B derive trom one gene by post-transcriptional processes involving RNA edition."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P23116: Q60697; 062162:
01-NOV-1991 (Rel. 20, Greated)
30-MAY 2000 (Rel. 39, Last sequence update)
10 MAY 2000 (Rel. 39, Last annotation update)
Edwaryotic translation initiation factor 3 subunit 10 (e1F·3 theta)
(E1F3 p167) (E1F3 p180) (E1F3 p185) (p162 protein) (Centrosomin).
                                                                                                                                                                                                                                                                                                                                         The coding sequences of unitaritied human genes. V. analysis of cDMA clones from genes (KiAA016; KIAA0200) deduced by analysis of cDMA clones from human cell line KG-1.";
                                                                            Homo Sapiens (Human).
Eukaryota, Metacoa: Chordata: Craniata; Vertebrata: Euteleostomi;
Mammalia, Eutheria, Frimates: Catarrhini; Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edkalyota, McCaroa, Choldata, Oraniata, Vertebrata, Bateleostomi;
Mammalia, Eutheria: Rodentia: Sciurognathi; Muridae; Musimae; Mus
                                                                                                                                                                                                                                                                              MEDLINE 96281124; PubMed 8724849;
Nagase T., Seki N., Ishikawa K.-I., lanaka A., Nomuta N.;
"Prediction of the coding sequences of unidentified human genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fisher R., Fillmore H., Reynolds A.H.; "Molecular cloning and characterization of the 162 kbu component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; tridels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a multi-protein complex phosphorylated by Sre.";
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
16-0CT-2001 (Rel. 40, Last annotation update) Hypothetical protein KIAA0182 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 514-961 FROM N.A (CENTROSOMIN B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 514-790 FROM N.A. (CENTROSOMIN A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 97;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY - PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY - ARG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110:2573-2578(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D80004; BAA11499.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.38;
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Best Local Similarity 64.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                              analysis of cDNA clones
DNA Res. 3:17 24(1996).
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1157 AA;
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                                                                                                                                                                                                                                                          TISSUE-Bone marrow;
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                       NCB1_Tax1D-9606;
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SEQUENCE
                                                          KIAA0182.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 X 10 AA TANDEM REPEAT OF D-[DE]-D-R-
[GP]-[PS]-[RW]-R-[GN]-{AM}.
RQEAKEHEKERILQEHEQIKKIVRERLEGIKTE ->
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EL -> DX (IN REF. 2 AND 3).
Q -> H (IN REF. 2 AND 3).
A -> V (IN REF. 2 AND 3).
                                                                                                                                                                                                           JOSWIG G., Petzelt C., Werner D.;
Submitted (DEC 1996) to the EMBL/GenBank/EDBJ databases.
-!- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF
MEDLINE-91277032; PubMed-1829085; Josewig G., Petzelt C., Werner D.; "Muzine cDMAs coding for the centrosomin A."; J. Cell Sci. 98:37-43(1991).
                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:95301; E1f3.
InterPro: IPR007071; PCT
InterPro: IPR002017; Spectrin.
Pfam; PF01899; PCI: I.
SMAR1; SM00088; PIN:: 1.
Initiation factor; Protein biosynthesis; Pepeal; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.3%; Score 43; DB 1; Length 1344; 50.0%; Pred. No. 1.1e+02; tive 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         793 793 E -> D (IN REF. 2).
1344 AA: 161949 MW: F4CAK2169F577712 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHSR -> SIVA (IN REF. 3).
E -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE EIF3S10 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U14172; AAA90910.1; · .
EMBL, X84651; CAA59144.1; - .
EMBL, X17373; CAA35246.1; - .
                                                                                                                                                                                                                                                                                                                   METHIONYL-TRNAI AND MRNA.
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CONFLICT
SEQUENCE
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Db 618 EREKERILQEHEGI 631
Scarch completed: January 16, 2003, 16:51:09
Job time: 22.4 secs

